



**Supplementary Figure 1.** Testing the power of the LCMS procedure to identify relationships among complex traits. Four causal models and one independent model are simulated as described in the text. The graphical representations for each simulated model are shown. Power is plotted as a function of the genetic correlation of the secondary trait. For each simulated model, the correlation between QTL genotypes and the primary trait,  $R_P$ , is fixed while the correlation between QTL genotypes and the secondary trait,  $R_S$ , varies from 0 up to the maximum allowed by the model. Holding the false positive rate fixed at 0.05, the power at each of the correlations considered between the QTL genotypes and secondary trait is computed. Highlighted in the power curve plot are lines indicating when the different models achieve 80% power to detect the true model. For causal models with the primary trait/QTL genotype correlations held fixed at 0.07, 0.10, and 0.20, we are at 80% power when the correlation between the secondary trait and QTL genotypes is approximately 0.015. For the other two simulated models we

are at 80% power when the correlation between QTL genotypes and the secondary trait is approximately 0.20.